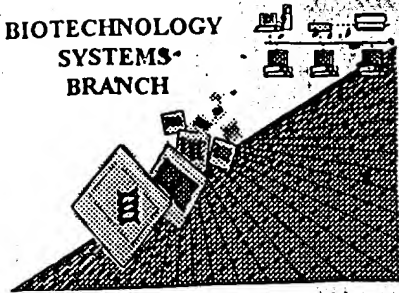


0590  
11/9

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/981900  
Source: OIP E  
Date Processed by STIC: 11/08/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/29/90

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 3<sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length.      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:37

Input Set : A:\es.txt

Output Set: N:\CRF3\11082001\I981900.raw

3 <110> APPLICANT: Sticklen, Masomeh B  
 4 Maqbool, Shahina B  
 5 Dale, Bruce E  
 7 <120> TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING LIGNINASE AND CELLULASE WHICH  
 DEGRADE LIGNIN  
 8 AND CELLULOSE TO FERMENTABLE SUGARS  
 10 <130> FILE REFERENCE: MSU 4.1-539  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/981,900  
 C--> 12 <141> CURRENT FILING DATE: 2001-10-18  
 12 <150> PRIOR APPLICATION NUMBER: 60/242,408  
 13 <151> PRIOR FILING DATE: 2000-10-20  
 15 <160> NUMBER OF SEQ ID NOS: 22  
 17 <170> SOFTWARE: PatentIn version 3.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1110  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Oryza sativa  
 24 <400> SEQUENCE: 1

25	gggtcggaga	tgccaccacg	gccacaaccc	acgagcccgg	cgcgacacca	ccgcgcgcgt	60
27	tgagccagcc	acaaacgccc	gcgcataggc	gcgccgcacg	cggccaatcc	taccacatcc	120
29	ccggcctccg	cggctcgagc	gccgtgccat	ccgatccgct	gagttttggc	tatttatacg	180
31	taccgcggga	gcctgtgtgc	agagagtga	tctcaagaag	tactcgagca	aagaaggaga	240
33	gagcttggtg	agctgcagag	atggccccct	ccgtgatggc	gtcgtcggcc	accaccgtcg	300
35	ctcccttcca	gggtcaagt	ccaccgccc	catgccgtcg	ccgcgcgtcc	gaactccagc	360
37	ttcggcaacg	tcagcatggc	ggcaggatca	ggtgcatgca	ggtaattacc	tactgatcca	420
39	acacacattc	ttcttcttct	ttcttcttct	aaccaacatt	aaccaacaac	tcaattatcg	480
41	tttattcatt	gaggtgtggc	cgattgaggg	catcaagaag	ttcgagaccc	tctcctacct	540
43	gccaccgctc	accgtggagg	acctcctgaa	gcagatcgag	tacctagctc	cgttccaagt	600
45	ggtgccctgc	ctcgagttca	gcaaggtcgg	atttgtctac	cgtgagaacc	acaagtcccc	660
47	tggatactac	gacggcaggt	actggaccat	gtggaagctg	cccatgttcg	ggtgcaccga	720
49	cgccacccag	gtcgtaagg	agctcgagga	ggccaagaag	gcgtaccctg	atgcattcgt	780
51	ccgtatcatc	ggcttcgaca	acgttaggca	ggtgcagctc	atcagcttca	tcgcctacaa	840
53	cccgggctgc	gaggagtctg	gtggcaacta	agccgtcctc	gtcatatata	gcctcgttta	900
55	attgttcatc	tctgattcga	tgatgtctcc	caccttggtt	cgtgtgttcc	cagtttggtt	960
57	catcgtcttt	tgattttacc	ggccgtgctc	tgcttttggt	ttttcttttc	acctgattct	1020
59	ctctctgact	tgatgtaaga	gtggtatctg	ctacgactat	atggtgtttg	ggtgaggcat	1080
61	atgtgaatga	aatctatgaa	agctccggct				1110
64	<210>	SEQ ID NO: 2					
65	<211>	LENGTH: 38					
66	<212>	TYPE: PRT					
67	<213>	ORGANISM: Oryza sativa					
69	<400>	SEQUENCE: 2					
71	Met	Ala	Pro	Ser	Val	Met	Ala
72	1		5			10	
75	Gln	Gly	Ser	Ser	Pro	Pro	Pro
76			20			25	
79	Gln	Leu	Arg	Gln	Arg	Gln	
80			35				

Does Not Comply  
 Corrected Diskette Needed

## RAW SEQUENCE LISTING

DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:37

Input Set : A:\es.txt

Output Set: N:\CRF3\11082001\I981900.raw

83 <210> SEQ ID NO: 3  
 84 <211> LENGTH: 6  
 85 <212> TYPE: PRT  
 86 <213> ORGANISM: synthetic peptide  
 88 <220> FEATURE:  
 89 <221> NAME/KEY: SIGNAL  
 90 <222> LOCATION: (1)..(6)  
 91 <223> OTHER INFORMATION: targets the peroxisomes of plants  
 94 <400> SEQUENCE: 3  
 96 Arg Ala Val Ala Arg Leu  
 97 1 5  
 100 <210> SEQ ID NO: 4  
 101 <211> LENGTH: 3004  
 102 <212> TYPE: DNA  
 103 <213> ORGANISM: Acidothermus cellulolyticus  
 105 <220> FEATURE:  
 106 <221> NAME/KEY: CDS  
 107 <222> LOCATION: (824)..(2512)  
 108 <223> OTHER INFORMATION: E I beta-1,4-endoglucanase precursor  
 111 <400> SEQUENCE: 4  
 112 ggatccacgt tgtacaaggt cacctgtccg tcgttctggt agagcggcgg gatggtcacc 60  
 114 cgcacgatct ctcccttgggt gatgtcgacg gtcacgtggt tacggtttgc ctcgcccgcg 120  
 116 attttcgcgc tcgggcttgc tccggctgtc gggttcggtt tggcgtggtg tgcggagcac 180  
 118 gccgaggcga tcccaatgag ggcaagggca agagcggagc cgatggcacg tcgggtggcc 240  
 120 gatggggtac gccgatgggg cgtggcgctc ccgcccgga cagaaccgga tgcggaatag 300  
 122 gtcacggtgc gacatgttgc cgtaccgagg acccggtatg caaggggtggg tgcgcgggtc 360  
 124 gcctgtgagc tgccggctgg cgtctggatc atgggaacga tcccaccatt ccccgcaatc 420  
 126 gacgcgatcg ggagcagggc ggcgcgagcc ggaccgtgtg gtcgagccgg acgatccgcc 480  
 128 catacgggtgc tgcaatgcc agcgccatgt tgtcaatccg ccaaatgcag caatgcacac 540  
 130 attggacagg attgtgactc tgagtaatga ttggattgcc ttcttgccgc ctacgcgtta 600  
 132 cgcagagtag gcgactgtat gcggtagggt ggcgctccag ccgtgggctg gacatgcctg 660  
 134 ctgcgaactc ttgacacgtc tggttgaacg cgcaatactc ccaacaccga tgggatcggt 720  
 136 cccataagtt tccgtctcac aacagaatcg gtgcgcctc atgatcaacg tgaaaggagt 780  
 138 acgggggaga acagacgggg gagaaaccaa cgggggattg gcg gtg ccg cgc gca 835  
 139 Val Pro Arg Ala  
 140 1  
 142 ttg cgg cga gtg cct ggc tgc cgg gtg atg ctg cgg gtc ggc gtc gtc 883  
 143 Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg Val Gly Val Val  
 144 5 10 15 20  
 146 gtc gcg gtg ctg gca ttg gtt gcc gca ctc gcc aac cta gcc gtg ccg 931  
 147 Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn Leu Ala Val Pro  
 148 25 30 35  
 150 cgg ccg gct cgc gcc gcg ggc ggc ggc tat tgg cac acg agc ggc cgg 979  
 151 Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His Thr Ser Gly Arg  
 152 40 45 50  
 154 gag atc ctg gac gcg aac aac gtg ccg gta cgg atc gcc ggc atc aac 1027  
 155 Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile Ala Gly Ile Asn  
 156 55 60 65  
 158 tgg ttt ggg ttc gaa acc tgc aat tac gtc gtg cac ggt ctc tgg tca 1075

*Entered Synthetic peptide is not a valid  
 213 response. "Artificial Sequence", "Unknown"  
 or the name of some particular species are  
 the only appropriate responses.*

## RAW SEQUENCE LISTING

DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:37

Input Set : A:\es.txt

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159	Trp	Phe	Gly	Phe	Glu	Thr	Cys	Asn	Tyr	Val	Val	His	Gly	Leu	Trp	Ser	
160		70					75					80					
162	cgc	gac	tac	cgc	agc	atg	ctc	gac	cag	ata	aag	tcg	ctc	ggc	tac	aac	1123
163	Arg	Asp	Tyr	Arg	Ser	Met	Leu	Asp	Gln	Ile	Lys	Ser	Leu	Gly	Tyr	Asn	
164	85					90					95					100	
166	aca	atc	cgg	ctg	ccg	tac	tct	gac	gac	att	ctc	aag	ccg	ggc	acc	atg	1171
167	Thr	Ile	Arg	Leu	Pro	Tyr	Ser	Asp	Asp	Ile	Leu	Lys	Pro	Gly	Thr	Met	
168					105					110					115		
170	ccg	aac	agc	atc	aat	ttt	tac	cag	atg	aat	cag	gac	ctg	cag	ggt	ctg	1219
171	Pro	Asn	Ser	Ile	Asn	Phe	Tyr	Gln	Met	Asn	Gln	Asp	Leu	Gln	Gly	Leu	
172				120					125					130			
174	acg	tcc	ttg	cag	gtc	atg	gac	aaa	atc	gtc	gcg	tac	gcc	ggt	cag	atc	1267
175	Thr	Ser	Leu	Gln	Val	Met	Asp	Lys	Ile	Val	Ala	Tyr	Ala	Gly	Gln	Ile	
176			135					140					145				
178	ggc	ctg	cgc	atc	att	ctt	gac	cgc	cac	cga	ccg	gat	tgc	agc	ggg	cag	1315
179	Gly	Leu	Arg	Ile	Ile	Leu	Asp	Arg	His	Arg	Pro	Asp	Cys	Ser	Gly	Gln	
180		150					155					160					
182	tcg	gcg	ctg	tgg	tac	acg	agc	agc	gtc	tcg	gag	gct	acg	tgg	att	tcc	1363
183	Ser	Ala	Leu	Trp	Tyr	Thr	Ser	Ser	Val	Ser	Glu	Ala	Thr	Trp	Ile	Ser	
184	165					170					175					180	
186	gac	ctg	caa	gcg	ctg	gcg	cag	cgc	tac	aag	gga	aac	ccg	acg	gtc	gtc	1411
187	Asp	Leu	Gln	Ala	Leu	Ala	Gln	Arg	Tyr	Lys	Gly	Asn	Pro	Thr	Val	Val	
188				185						190					195		
190	ggc	ttt	gac	ttg	cac	aac	gag	ccg	cat	gac	ccg	gcc	tgc	tgg	ggc	tgc	1459
191	Gly	Phe	Asp	Leu	His	Asn	Glu	Pro	His	Asp	Pro	Ala	Cys	Trp	Gly	Cys	
192			200						205				210				
194	ggc	gat	ccg	agc	atc	gac	tgg	cga	ttg	gcc	gcc	gag	ccg	gcc	gga	aac	1507
195	Gly	Asp	Pro	Ser	Ile	Asp	Trp	Arg	Leu	Ala	Ala	Glu	Arg	Ala	Gly	Asn	
196			215					220					225				
198	gcc	gtg	ctc	tcg	gtg	aat	ccg	aac	ctg	ctc	att	ttc	gtc	gaa	ggt	gtg	1555
199	Ala	Val	Leu	Ser	Val	Asn	Pro	Asn	Leu	Leu	Ile	Phe	Val	Glu	Gly	Val	
200		230					235					240					
202	cag	agc	tac	aac	gga	gac	tcc	tac	tgg	tgg	ggc	ggc	aac	ctg	caa	gga	1603
203	Gln	Ser	Tyr	Asn	Gly	Asp	Ser	Tyr	Trp	Trp	Gly	Gly	Asn	Leu	Gln	Gly	
204	245					250					255					260	
206	gcc	ggc	cag	tac	ccg	gtc	gtg	ctg	aac	gtg	ccg	aac	cgc	ctg	gtg	tac	1651
207	Ala	Gly	Gln	Tyr	Pro	Val	Val	Leu	Asn	Val	Pro	Asn	Arg	Leu	Val	Tyr	
208				265					270				275				
210	tcg	gcg	cac	gac	tac	gcg	acg	agc	gtc	tac	ccg	cag	acg	tgg	ttc	agc	1699
211	Ser	Ala	His	Asp	Tyr	Ala	Thr	Ser	Val	Tyr	Pro	Gln	Thr	Trp	Phe	Ser	
212				280					285				290				
214	gat	ccg	acc	ttc	ccc	aac	aac	atg	ccc	ggc	atc	tgg	aac	aag	aac	tgg	1747
215	Asp	Pro	Thr	Phe	Pro	Asn	Asn	Met	Pro	Gly	Ile	Trp	Asn	Lys	Asn	Trp	
216			295					300					305				
218	gga	tac	ctc	ttc	aat	cag	aac	att	gca	ccg	gta	tgg	ctg	ggc	gaa	ttc	1795
219	Gly	Tyr	Leu	Phe	Asn	Gln	Asn	Ile	Ala	Pro	Val	Trp	Leu	Gly	Glu	Phe	
220		310					315					320					
222	ggt	acg	aca	ctg	caa	tcc	acg	acc	gac	cag	acg	tgg	ctg	aag	acg	ctc	1843
223	Gly	Thr	Thr	Leu	Gln	Ser	Thr	Thr	Asp	Gln	Thr	Trp	Leu	Lys	Thr	Leu	

## RAW SEQUENCE LISTING

DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:37

Input Set : A:\es.txt

Output Set: N:\CRF3\11082001\I981900.raw

224	325		330		335		340	
226	gtc	cag	tac	cta	cgg	ccg	acc	gcg
227	Val	Gln	Tyr	Leu	Arg	Pro	Thr	Ala
228								
230	tgg	acc	ttc	tgg	tcc	tgg	aac	ccc
231	Trp	Thr	Phe	Trp	Ser	Trp	Asn	Pro
232								
234	ctc	aag	gat	gac	tgg	cag	acg	gtc
235	Leu	Lys	Asp	Asp	Trp	Gln	Thr	Val
236								
238	gcg	ccg	atc	aag	tcg	tcg	att	ttc
239	Ala	Pro	Ile	Lys	Ser	Ser	Ile	Phe
240								
242	cct	agc	agt	caa	ccg	tcc	ccg	tcg
243	Pro	Ser	Ser	Gln	Pro	Ser	Pro	Ser
244	405							
246	ccg	tcg	gcg	agt	cgg	acg	ccg	acg
247	Pro	Ser	Ala	Ser	Arg	Thr	Pro	Thr
248								
250	ccg	acg	cca	acg	ctg	acc	cct	act
251	Pro	Thr	Pro	Thr	Leu	Thr	Pro	Thr
252								
254	ccg	acg	ccg	tca	ccg	acg	gca	gcc
255	Pro	Thr	Pro	Ser	Pro	Thr	Ala	Ala
256								
258	tac	cag	gtc	aac	agc	gat	tgg	ggc
259	Tyr	Gln	Val	Asn	Ser	Asp	Trp	Gly
260								
262	gtg	aca	aat	tcc	gga	tcc	gtc	gcg
263	Val	Thr	Asn	Ser	Gly	Ser	Val	Ala
264	485							
266	aca	ttc	ggc	gga	aat	cag	acg	att
267	Thr	Phe	Gly	Gly	Asn	Gln	Thr	Ile
268								
270	acg	cag	aac	ggg	cag	tcg	gta	acg
271	Thr	Gln	Asn	Gly	Gln	Ser	Val	Thr
272								
274	gtg	att	cag	cct	ggg	cag	aac	acc
275	Val	Ile	Gln	Pro	Gly	Gln	Asn	Thr
276								
278	acc	gga	agc	aac	gcg	gca	ccg	aca
279	Thr	Gly	Ser	Asn	Ala	Ala	Pro	Thr
280								
282	tacgtcgggg	agccgacggg	aggggtccgga	ccgtcgggttc	cccggcttcc	acctatggag		
284	cgaacccaac	aatccggacg	gaactgcagg	taccagagag	gaacgacacg	aatgcccgc		
286	atctcaaaac	ggctgcgagc	cggcgtcctc	gccggggcgg	tgagcatcgc	agcctccatc		
288	gtgcgctgg	cgatgcagca	tcctgccatc	gccgcgacgc	acgtcgacaa	tcctatgcg		
290	ggagcgacct	tcttcgtcaa	cccgtactgg	gcgcaagaag	tacagagcga	acggcgaacc		
292	agaccaatgc	cactctcgca	gcgaaaatgc	gcgtcgtttc	cacatattcg	acggccgtct		

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DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:37

Input Set : A:\es.txt

Output Set: N:\CRF3\11082001\I981900.raw

```

294 ggatggaccg catcgtgcg atcaacggcg tcaacggcgg acccggcttg acgacatc 2932
296 tggacgccgc cctctcccag cagcagggaa ccaccctga agtcattgag attgtcatc 2992
298 acgatctgcc gg 3004
301 <210> SEQ ID NO: 5
302 <211> LENGTH: 562
303 <212> TYPE: PRT
304 <213> ORGANISM: Acidothermus cellulolyticus
306 <400> SEQUENCE: 5
308 Val Pro Arg Ala Leu Arg Arg Val Pro Gly Ser Arg Val Met Leu Arg
309 1 5 10 15
312 Val Gly Val Val Ala Val Leu Ala Leu Val Ala Ala Leu Ala Asn
313 20 25 30
316 Leu Ala Val Pro Arg Pro Ala Arg Ala Ala Gly Gly Gly Tyr Trp His
317 35 40 45
320 Thr Ser Gly Arg Glu Ile Leu Asp Ala Asn Asn Val Pro Val Arg Ile
321 50 55 60
324 Ala Gly Ile Asn Trp Phe Gly Phe Glu Thr Cys Asn Tyr Val Val His
325 65 70 75 80
328 Gly Leu Trp Ser Arg Asp Tyr Arg Ser Met Leu Asp Gln Ile Lys Ser
329 85 90 95
332 Leu Gly Tyr Asn Thr Ile Arg Leu Pro Tyr Ser Asp Asp Ile Leu Lys
333 100 105 110
336 Pro Gly Thr Met Pro Asn Ser Ile Asn Phe Tyr Gln Met Asn Gln Asp
337 115 120 125
340 Leu Gln Gly Leu Thr Ser Leu Gln Val Met Asp Lys Ile Val Ala Tyr
341 130 135 140
344 Ala Gly Gln Ile Gly Leu Arg Ile Ile Leu Asp Arg His Arg Pro Asp
345 145 150 155 160
348 Cys Ser Gly Gln Ser Ala Leu Trp Tyr Thr Ser Ser Val Ser Glu Ala
349 165 170 175
352 Thr Trp Ile Ser Asp Leu Gln Ala Leu Ala Gln Arg Tyr Lys Gly Asn
353 180 185 190
356 Pro Thr Val Val Gly Phe Asp Leu His Asn Glu Pro His Asp Pro Ala
357 195 200 205
360 Cys Trp Gly Cys Gly Asp Pro Ser Ile Asp Trp Arg Leu Ala Ala Glu
361 210 215 220
364 Arg Ala Gly Asn Ala Val Leu Ser Val Asn Pro Asn Leu Leu Ile Phe
365 225 230 235 240
368 Val Glu Gly Val Gln Ser Tyr Asn Gly Asp Ser Tyr Trp Trp Gly Gly
369 245 250 255
372 Asn Leu Gln Gly Ala Gly Gln Tyr Pro Val Val Leu Asn Val Pro Asn
373 260 265 270
376 Arg Leu Val Tyr Ser Ala His Asp Tyr Ala Thr Ser Val Tyr Pro Gln
377 275 280 285
380 Thr Trp Phe Ser Asp Pro Thr Phe Pro Asn Asn Met Pro Gly Ile Trp
381 290 295 300
384 Asn Lys Asn Trp Gly Tyr Leu Phe Asn Gln Asn Ile Ala Pro Val Trp
385 305 310 315 320
388 Leu Gly Glu Phe Gly Thr Thr Leu Gln Ser Thr Thr Asp Gln Thr Trp

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 11/08/2001

PATENT APPLICATION: US/09/981,900

TIME: 13:18:38

Input Set : A:\es.txt

Output Set: N:\CRF3\11082001\I981900.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7